

PRODUCTION OF GAMMA LINOLENIC ACID
BY A $\Delta 6$ -DESATURASE

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This is a continuation-in-part of U.S. Serial
No. 08/789,936 filed January 28, 1997 which is a
continuation-in-part of U.S. Serial No. 08/307,382,
5 filed September 14, 1994 which is a continuation of U.S.
Serial No. 07/959,952 filed October 13, 1992 which is a
continuation-in-part of U.S. Serial No. 817,919, filed
January 8, 1992, which is a continuation-in-part
application of U.S. Serial No. 774,475 filed October 10,
10 ~~1991.~~

FIELD OF THE INVENTION

Linoleic acid (18:2) (LA) is transformed into
gamma linolenic acid (18:3) (GLA) by the enzyme $\Delta 6$ -
15 desaturase. When this enzyme, or the nucleic acid
encoding it, is transferred into LA-producing cells, GLA
is produced. The present invention provides nucleic
acids comprising the $\Delta 6$ -desaturase gene. More
specifically, the nucleic acids comprise the promoters,
20 coding regions and termination regions of the $\Delta 6$ -
desaturase genes. The present invention is further
directed to recombinant constructions comprising a $\Delta 6$ -
desaturase coding region in functional combination with
heterologous regulatory sequences. The nucleic acids
25 and recombinant constructions of the instant invention
are useful in the production of GLA in transgenic
organisms.

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BACKGROUND OF THE INVENTION

1 Unsaturated fatty acids such as linoleic
 ($C_{18}\Delta^{9,12}$) and α -linolenic ($C_{18}\Delta^{9,12,15}$) acids are essential
 dietary constituents that cannot be synthesized by
 vertebrates since vertebrate cells can introduce double
5 bonds at the Δ^9 position of fatty acids but cannot
 introduce additional double bonds between the Δ^9 double
 bond and the methyl-terminus of the fatty acid chain.
 Because they are precursors of other products, linoleic
 and α -linolenic acids are essential fatty acids, and are
10 usually obtained from plant sources. Linoleic acid can
 be converted by mammals into γ -linolenic acid (GLA,
 $C_{18}\Delta^{6,9,12}$) which can in turn be converted to arachidonic
 acid (20:4), a critically important fatty acid since it
 is an essential precursor of most prostaglandins.
15 The dietary provision of linoleic acid, by
 virtue of its resulting conversion to GLA and
 arachidonic acid, satisfies the dietary need for GLA and
 arachidonic acid. However, a relationship has been
 demonstrated between consumption of saturated fats and
20 health risks such as hypercholesterolemia,
 atherosclerosis and other clinical disorders which
 correlate with susceptibility to coronary disease, while
 the consumption of unsaturated fats has been associated
 with decreased blood cholesterol concentration and
25 reduced risk of atherosclerosis. The therapeutic
 benefits of dietary GLA may result from GLA being a
 precursor to arachidonic acid and thus subsequently
 contributing to prostaglandin synthesis. Accordingly,

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consumption of the more unsaturated GLA, rather than
1 linoleic acid, has potential health benefits. However,
GLA is not present in virtually any commercially grown
crop plant.

Linoleic acid is converted into GLA by the
5 enzyme $\Delta 6$ -desaturase. $\Delta 6$ -desaturase, an enzyme of more
than 350 amino acids, has a membrane-bound domain and an
active site for desaturation of fatty acids. When this
enzyme is transferred into cells which endogenously
produce linoleic acid but not GLA, GLA is produced. The
10 present invention, by providing genes encoding $\Delta 6$ -
desaturase, allows the production of transgenic
organisms which contain functional $\Delta 6$ -desaturase and
which produce GLA. In addition to allowing production
of large amounts of GLA, the present invention provides
15 new dietary sources of GLA.

SUMMARY OF THE INVENTION

The present invention is directed to isolated
 $\Delta 6$ -desaturase genes. Specifically, the isolated genes
20 comprise the $\Delta 6$ -desaturase promoters, coding regions,
and termination regions.

The present invention is further directed to
expression vectors comprising the $\Delta 6$ -desaturase
promoter, coding region and termination region.

25 Yet another aspect of this invention is
directed to expression vectors comprising a $\Delta 6$ -
desaturase coding region in functional combination with

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heterologous regulatory regions, i.e. elements not
1 derived from the $\Delta 6$ -desaturase gene.

Cells and organisms comprising the vectors of
the present invention, and progeny of such organisms,
are also provided by the present invention.

5 A further aspect of the present invention
provides isolated bacterial $\Delta 6$ -desaturase. Isolated
plant $\Delta 6$ -desaturases are also provided.

Yet another aspect of this invention provides
a method for producing plants with increased gamma
10 linolenic acid content.

A method for producing chilling tolerant
plants is also provided by the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS:

15 Fig. 1 depicts the hydropathy profiles of the
deduced amino acid sequences of Synechocystis $\Delta 6$ -
desaturase (Panel A) and $\Delta 12$ -desaturase (Panel B).
Putative membrane spanning regions are indicated by
solid bars. Hydrophobic index was calculated for a
20 window size of 19 amino acid residues [Kyte, et al.
(1982) J. Molec. Biol. 157].

Fig. 2 provides gas liquid chromatography
profiles of wild type (Panel A) and transgenic (Panel B)
Anabaena.

25 Fig. 3 is a diagram of maps of cosmid cSy75,
cSy13 and Csy7 with overlapping regions and subclones.
The origins of subclones of Csy75, Csy75-3.5 and Csy7

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are indicated by the dashed diagonal lines. Restriction
1 sites that have been inactivated are in parentheses.

Fig. 4 provides gas liquid chromatography
profiles of wild type (Panel A) and transgenic (Panel B)
tobacco.

5 Fig. 5A depicts the DNA sequence of a $\Delta 6$ -
desaturase cDNA isolated from borage.

Fig. 5B depicts the protein sequence of the
open reading frame in the isolated borage $\Delta 6$ -desaturase
cDNA. Three amino acid motifs characteristic of
10 desaturases are indicated and are, in order, lipid box,
metal box 1, and metal box 2.

Fig. 6 is a dendrogram showing similarity of
the borage $\Delta 6$ -desaturase to other membrane-bound
desaturases. The amino acid sequence of the borage $\Delta 6$ -
15 desaturase was compared to other known desaturases using
Gene Works (IntelliGenetics). Numerical values
correlate to relative phylogenetic distances between
subgroups compared.

Fig. 7 is a restriction map of 221. $\Delta 6$.NOS and
20 121. $\Delta 6$.NOS. In 221. $\Delta 6$.NOS, the remaining portion of the
plasmid is pBI221 and in 121. $\Delta 6$.NOS, the remaining
portion of the plasmid is pBI121.

Fig. 8 provides gas liquid chromatography
profiles of mock transfected (Panel A) and 221. $\Delta 6$.NOS
25 transfected (Panel B) carrot cells. The positions of
18:2, 18:3 α , and 18:3 γ (GLA) are indicated.

Fig. 9 provides gas liquid chromatography
profiles of an untransformed tobacco leaf (Panel A) and

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a tobacco leaf transformed with 121.Δ6.NOS. The
1 positions of 18:2, 18:3 a, 18:3γ (GLA), and 18:4 are
indicated.

Fig. 10 is the complete DNA sequence and
deduced amino acid sequence of evening primrose Δ6-
5 desaturase. A heme binding motif of cytochrome b5
proteins is indicated by underlined bold text.
Underlined plain text indicates three histine rich
motifs (HRMs). The motifs in this sequence are
identical to those found in borage Δ6-desaturase with
10 the exception of those that are italicized (S 161 and L
374).

Fig. 11 is a formatted alignment of the
evening primrose and borage Δ6-desaturase amino acid
sequences.

15 Fig. 12A is a Kyte-Doolittle hydrophobicity
plot for borage Δ6-desaturase.

Fig. 12B is a Kyte-Doolittle hydrophobicity
plot for evening primrose Δ6-desaturase.

Fig. 13A is a Hopwood hydrophobicity plot for
20 borage Δ6-desaturase. The y axis is a normalized
parameter that estimates hydrophobicity; that the x axis
represents the linear amino acid sequences.

Fig. 13B is a Hopwood hydrophobicity plot for
evening primrose Δ6-desaturase. X and y axes are as in
25 Figure 13A.

Fig. 14A graphically depicts the location of
the transmembrane regions for borage Δ6-desaturase.
Positive values (y-axis) greater than 500 are considered

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significant predictors of a membrane spanning region.

1 The x-axis represents the linear amino acid sequences.

Fig. 14B graphically depicts the location of the transmembrane regions for evening primrose $\Delta 6$ -desaturase. X and y axes are as in Figure 14A.

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DETAILED DESCRIPTION OF THE INVENTION:

The present invention provides isolated nucleic acids encoding $\Delta 6$ -desaturase. To identify a nucleic acid encoding $\Delta 6$ -desaturase, DNA is isolated from an organism which produces GLA. Said organism can be, for example, an animal cell, certain fungi (e.g. Mortierella), certain bacteria (e.g. Synechocystis) or certain plants (borage, Oenothera, currants). The isolation of genomic DNA can be accomplished by a variety of methods well-known to one of ordinary skill in the art, as exemplified by Sambrook et al. (1989) in Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, NY. The isolated DNA is fragmented by physical methods or enzymatic digestion and cloned into an appropriate vector, e.g. a bacteriophage or cosmid vector, by any of a variety of well-known methods which can be found in references such as Sambrook et al. (1989). Expression vectors containing the DNA of the present invention are specifically contemplated herein.

25 DNA encoding Δ -desaturase can be identified by gain of function analysis. The vector containing fragmented DNA is transferred, for example by infection, transconjugation, transfection, into a host organism

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that produces linoleic acid but not GLA. As used
1 herein, "transformation" refers generally to the
incorporation of foreign DNA into a host cell. Methods
for introducing recombinant DNA into a host organism are
known to one of ordinary skill in the art and can be
5 found, for example, in Sambrook et al. (1989).
Production of GLA by these organisms (i.e., gain of
function) is assayed, for example by gas chromatography
or other methods known to the ordinarily skilled
artisan. Organisms which are induced to produce GLA,
10 i.e. have gained function by the introduction of the
vector, are identified as expressing DNA encoding Δ -
desaturase, and said DNA is recovered from the
organisms. The recovered DNA can again be fragmented,
cloned with expression vectors, and functionally
15 assessed by the above procedures to define with more
particularity the DNA encoding $\Delta 6$ -desaturase.

As an example of the present invention, random
DNA is isolated from the cyanobacteria Synechocystis
Pasteur Culture Collection (PCC) 6803, American Type
20 Culture Collection (ATCC) 27184, cloned into a cosmid
vector, and introduced by transconjugation into the GLA-
deficient Cyanobacterium Anabaena strain PCC 7120, ATCC
27893. Production of GLA from Anabaena linoleic acid is
monitored by gas chromatography and the corresponding
25 DNA fragment is isolated.

The isolated DNA is sequenced by methods well-
known to one of ordinary skill in the art as found, for
example, in Sambrook et al. (1989).

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In accordance with the present invention, DNA molecules comprising $\Delta 6$ -desaturase genes have been isolated. More particularly, a 3.588 kilobase (kb) DNA comprising a $\Delta 6$ -desaturase gene has been isolated from the cyanobacteria Synechocystis. The nucleotide sequence of the 3.588 kb DNA was determined and is shown in SEQ ID NO:1. Open reading frames defining potential coding regions are present from nucleotide 317 to 1507 and from nucleotide 2002 to 3081. To define the nucleotides responsible for encoding $\Delta 6$ -desaturase, the 3.588 kb fragment that confers $\Delta 6$ -desaturase activity is cleaved into two subfragments, each of which contains only one open reading frame. Fragment ORF1 contains nucleotides 1 through 1704, while fragment ORF2 contains nucleotides 1705 through 3588. Each fragment is subcloned in both forward and reverse orientations into a conjugal expression vector (AM542, Wolk *et al.* [1984] Proc. Natl. Acad. Sci. USA 81, 1561) that contains a cyanobacterial carboxylase promoter. The resulting constructs (i.e. ORF1(F), ORF1(R), ORF2(F) and ORF2(R)) are conjugated to wild-type Anabaena PCC 7120 by standard methods (see, for example, Wolk *et al.* (1984) Proc. Natl. Acad. Sci. USA 81, 1561). Conjugated cells of Anabaena are identified as Neo^R green colonies on a brown background of dying non-conjugated cells after two weeks of growth on selective media (standard mineral media BG11N + containing 30 μ g/ml of neomycin according to Rippka *et al.*, (1979) J. Gen Microbiol. 111, 1). The green colonies are selected and grown in selective

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liquid media (BG11N + with 15 μ g/ml neomycin). Lipids
 1 are extracted by standard methods (e.g. Dahmer et al.,
 (1989) Journal of American Oil Chemical Society 66, 543)
 from the resulting transconjugants containing the
 forward and reverse oriented ORF1 and ORF2 constructs.
 5 For comparison, lipids are also extracted from wild-type
 cultures of Anabaena and Synechocystis. The fatty acid
 methyl esters are analyzed by gas liquid chromatography
 (GLC), for example with a Tracor-560 gas liquid
 chromatograph equipped with a hydrogen flame ionization
 10 detector and a capillary column. The results of GLC
 analysis are shown in Table 1.

Table 1: Occurrence of C18 fatty acids in wild-type and
 transgenic cyanobacteria

15	SOURCE	18:0	18:1	18:2	18:3	22:6	18:4
	Anabaena (wild type)	+	+	+	-	+	-
	Anabaena + ORF1 (F)	+	+	+	-	+	-
	Anabaena + ORF1 (R)	+	+	+	-	+	-
20	Anabaena + ORF2 (F)	+	+	+	+	+	+
	Anabaena + ORF2 (R)	+	+	+	-	+	-
	Synechocystis (wild type)	+	+	+	+	-	-

25 As assessed by GLC analysis, GLA deficient
Anabaena gain the function of GLA production when the
 construct containing ORF2 in forward orientation is
 introduced by transconjugation. Transconjugants

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containing constructs with ORF2 in reverse orientation
1 to the carboxylase promoter, or ORF1 in either
orientation, show no GLA production. This analysis
demonstrates that the single open reading frame (ORF2)
within the 1884 bp fragment encodes $\Delta 6$ -desaturase. The
5 1884 bp fragment is shown as SEQ ID NO:3. This is
substantiated by the overall similarity of the
hydropathy profiles between $\Delta 6$ -desaturase and $\Delta 12$ -
desaturase [Wada et al. (1990) Nature 347] as shown in
Fig. 1 as (A) and (B), respectively.

10 Also in accordance with the present invention,
a cDNA comprising a $\Delta 6$ -desaturase gene from borage
(Borago officinalis) has been isolated. The nucleotide
sequence of the 1.685 kilobase (kb) cDNA was determined
and is shown in Fig. 5A (SEQ ID NO: 4). The ATG start
15 codon and stop codon are underlined. The amino acid
sequence corresponding to the open reading frame in the
borage delta 6-desaturase is shown in Fig. 5B (SEQ ID
NO: 5).

20 Additionally, the present invention provides a
 $\Delta 6$ -desaturase gene from evening primrose (Oenothera
biennis). The nucleotide sequence of the 1.687 kb cDNA
was determined and is depicted in Figure 10 (SEQ ID
NO:26). Also shown in Figure 10 is the deduced amino
acid sequence of evening primrose $\Delta 6$ -desaturase.

25 Isolated nucleic acids encoding $\Delta 6$ -desaturase
can be identified from other GLA-producing organisms by
the gain of function analysis described above, or by
nucleic acid hybridization techniques using the isolated
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1 nucleic acid which encodes Synechocystis, borage, or
evening primrose $\Delta 6$ -desaturase as a hybridization probe.
Both methods are known to the skilled artisan and are
contemplated by the present invention. The
hybridization probe can comprise the entire DNA sequence
5 disclosed as SEQ. ID NO:1 or SEQ. ID NO:4, or a
restriction fragment or other DNA fragment thereof,
including an oligonucleotide probe. Methods for cloning
homologous genes by cross-hybridization are known to the
ordinarily skilled artisan and can be found, for
10 example, in Sambrook (1989) and Beltz *et al.* (1983)
Methods in Enzymology 100, 266.

In another method of identifying a delta 6-
desaturase gene from an organism producing GLA, a cDNA
library is made from poly-A⁺ RNA isolated from polysomal
15 RNA. In order to eliminate hyper-abundant expressed
genes from the cDNA population, cDNAs or fragments
thereof corresponding to hyper-abundant cDNAs genes are
used as hybridization probes to the cDNA library. Non
hybridizing plaques are excised and the resulting
20 bacterial colonies are used to inoculate liquid cultures
and sequenced. For example, as a means of eliminating
other seed storage protein cDNAs from a cDNA library
made from borage polysomal RNA, cDNAs corresponding to
abundantly expressed seed storage proteins are first
25 hybridized to the cDNA library. The "subtracted" DNA
library is then used to generate expressed sequence tags
(ETSS) and such tags are used to scan a data base such
as GenBank to identify potential desaturates.

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Using another method, an evening primrose cDNA
1 may be isolated by first synthesizing sequences from the
borage $\Delta 6$ -desaturase gene and then using these sequences
as primers in a PCR reaction with the evening primrose
cDNA library serving as template. PCR fragments of
5 expected size may then be used to screen an evening
primrose cDNA library. Hybridizing clones may then be
sequenced and compared to the borage cDNA sequence to
determine if the hybridizing clone represents an evening
primrose $\Delta 6$ -desaturase gene.

10 Transgenic organisms which gain the function
of GLA production by introduction of DNA encoding $\Delta 6$ -
desaturase also gain the function of octadecatetraenoic
acid (18:4^{6,9,12,15}) production. Octadecatetraenoic acid
is present normally in fish oils and in some plant
15 species of the Boraginaceae family (Craig et al. [1964]
J. Amer. Oil Chem. Soc. 41, 209-211; Gross et al. [1976]
Can. J. Plant Sci. 56, 659-664). In the transgenic
organisms of the present invention, octadecatetraenoic
acid results from further desaturation of α -linolenic
20 acid by $\Delta 6$ -desaturase or desaturation of GLA by $\Delta 15$ -
desaturase.

The 359 amino acids encoded by ORF2, i.e. the
open reading frame encoding Synechocystis $\Delta 6$ -desaturase,
are shown as SEQ. ID NO:2. The open reading frame
25 encoding the borage $\Delta 6$ -desaturase is shown in SEQ ID NO:
5. The present invention further contemplates other
nucleotide sequences which encode the amino acids of SEQ
ID NO:2 and SEQ ID NO: 5. It is within the ken of the

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ordinarily skilled artisan to identify such sequences
1 which result, for example, from the degeneracy of the
genetic code. Furthermore, one of ordinary skill in the
art can determine, by the gain of function analysis
described hereinabove, smaller subfragments of the
5 fragments containing the open reading frames which
encode $\Delta 6$ -desaturases.

The present invention contemplates any such
polypeptide fragment of $\Delta 6$ -desaturase and the nucleic
acids therefor which retain activity for converting LA
10 to GLA.

In another aspect of the present invention, a
vector containing a nucleic acid of the present
invention or a smaller fragment containing the promoter,
coding sequence and termination region of a $\Delta 6$ -
15 desaturase gene is transferred into an organism, for
example, cyanobacteria, in which the $\Delta 6$ -desaturase
promoter and termination regions are functional.
Accordingly, organisms producing recombinant $\Delta 6$ -
desaturase are provided by this invention. Yet another
20 aspect of this invention provides isolated $\Delta 6$ -
desaturase, which can be purified from the recombinant
organisms by standard methods of protein purification.
(For example, see Ausubel et al. [1987] Current
Protocols in Molecular Biology, Green Publishing
25 Associates, New York).

Vectors containing DNA encoding $\Delta 6$ -desaturase
are also provided by the present invention. It will be
apparent to one of ordinary skill in the art that

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appropriate vectors can be constructed to direct the
1 expression of the $\Delta 6$ -desaturase coding sequence in a
variety of organisms. Replicable expression vectors are
particularly preferred. Replicable expression vectors
as described herein are DNA or RNA molecules engineered
5 for controlled expression of a desired gene, i.e. the
 $\Delta 6$ -desaturase gene. Preferably the vectors are
plasmids, bacteriophages, cosmids or viruses. Shuttle
vectors, e.g. as described by Wolk *et al.* (1984) Proc.
Natl. Acad. Sci. USA, 1561-1565 and Bustos *et al.* (1991)
10 J. Bacteriol. 174, 7525-7533, are also contemplated in
accordance with the present invention. Sambrook *et al.*
(1989), Goeddel, ed. (1990) Methods in Enzymology 185
Academic Press, and Perbal (1988) A Practical Guide to
Molecular Cloning, John Wiley and Sons, Inc., provide
15 detailed reviews of vectors into which a nucleic acid
encoding the present $\Delta 6$ -desaturase can be inserted and
expressed. Such vectors also contain nucleic acid
sequences which can effect expression of nucleic acids
encoding $\Delta 6$ -desaturase. Sequence elements capable of
20 effecting expression of a gene product include
promoters, enhancer elements, upstream activating
sequences, transcription termination signals and
polyadenylation sites. The upstream 5' untranslated
region of the evening primrose $\Delta 6$ -desaturase gene as
25 depicted in Figure 10 may also be used. Both
constitutive and tissue specific promoters are
contemplated. For transformation of plant cells, the
cauliflower mosaic virus (CaMV) 35S promoter, other

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constitutive promoters and promoters which are regulated
1 during plant seed maturation are of particular interest.
All such promoter and transcriptional regulatory
elements, singly or in combination, are contemplated for
use in the present replicable expression vectors and are
5 known to one of ordinary skill in the art. The CaMV 35S
promoter is described, for example, by Restrepo et al.
(1990) Plant Cell 2, 987. Genetically engineered and
mutated regulatory sequences are also contemplated.

The ordinarily skilled artisan can determine
10 vectors and regulatory elements suitable for expression
in a particular host cell. For example, a vector
comprising the promoter from the gene encoding the
carboxylase of Anabaena operably linked to the coding
region of $\Delta 6$ -desaturase and further operably linked to a
15 termination signal from Synechocystis is appropriate for
expression of $\Delta 6$ -desaturase in cyanobacteria. "Operably
linked" in this context means that the promoter and
terminator sequences effectively function to regulate
transcription. As a further example, a vector
20 appropriate for expression of $\Delta 6$ -desaturase in
transgenic plants can comprise a seed-specific promoter
sequence derived from helianthinin, napin, or glycinin
operably linked to the $\Delta 6$ -desaturase coding region and
further operably linked to a seed termination signal or
25 the nopaline synthase termination signal. As a still
further example, a vector for use in expression of $\Delta 6$ -
desaturase in plants can comprise a constitutive
promoter or a tissue specific promoter operably linked

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to the $\Delta 6$ -desaturase coding region and further operably
1 linked to a constitutive or tissue specific terminator
or the nopaline synthase termination signal.

In particular, the helianthinin regulatory
elements disclosed in applicant's copending U.S.
5 Application Serial No. 682,354, filed April 8, 1991 and
incorporated herein by reference, are contemplated as
promoter elements to direct the expression of the $\Delta 6$ -
desaturases of the present invention. The albumin
regulatory elements disclosed in applicant's copending
10 U.S. application Serial No. 08/831,570 and the oleosin //
regulatory elements disclosed in applicant's copending //
U.S. application Serial No. 08/831,575 (both applications 13
filed April 9, 1997), and incorporated herein by 14
reference, are also contemplated as elements to direct
15 the expression of the $\Delta 6$ -desaturases of the present
invention.

Modifications of the nucleotide sequences or
regulatory elements disclosed herein which maintain the
functions contemplated herein are within the scope of
20 this invention. Such modifications include insertions,
substitutions and deletions, and specifically
substitutions which reflect the degeneracy of the
genetic code.

Standard techniques for the construction of
25 such hybrid vectors are well-known to those of ordinary
skill in the art and can be found in references such as
Sambrook et al. (1989), or any of the myriad of
laboratory manuals on recombinant DNA technology that

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are widely available. A variety of strategies are
1 available for ligating fragments of DNA, the choice of
which depends on the nature of the termini of the DNA
fragments. It is further contemplated in accordance
with the present invention to include in the hybrid
5 vectors other nucleotide sequence elements which
facilitate cloning, expression or processing, for
example sequences encoding signal peptides, a sequence
encoding KDEL or related sequence, which is required for
retention of proteins in the endoplasmic reticulum or
10 sequences encoding transit peptides which direct $\Delta 6$ -
desaturase to the chloroplast. Such sequences are known
to one of ordinary skill in the art. An optimized
transit peptide is described, for example, by Van den
Broeck *et al.* (1985) Nature 313, 358. Prokaryotic and
15 eukaryotic signal sequences are disclosed, for example,
by Michaelis *et al.* (1982) Ann. Rev. Microbiol. 36, 425.

A further aspect of the instant invention
provides organisms other than cyanobacteria or plants
which contain the DNA encoding the $\Delta 6$ -desaturase of the
20 present invention. The transgenic organisms
contemplated in accordance with the present invention
include bacteria, cyanobacteria, fungi, and plants and
animals. The isolated DNA of the present invention can
be introduced into the host by methods known in the art,
25 for example infection, transfection, transformation or
transconjugation. Techniques for transferring the DNA
of the present invention into such organisms are widely

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known and provided in references such as Sambrook et al.
1 (1989).

A variety of plant transformation methods are
known. The $\Delta 6$ -desaturase gene can be introduced into
plants by a leaf disk transformation-regeneration
5 procedure as described by Horsch et al. (1985) Science
227, 1229. Other methods of transformation, such as
protoplast culture (Horsch et al. (1984) Science 223,
496; DeBlock et al. (1984) EMBO J. 2, 2143; Barton et
al. (1983) Cell 32, 1033) can also be used and are
10 within the scope of this invention. In a preferred
embodiment plants are transformed with Agrobacterium-
derived vectors such as those described in Klett et al.
(1987) Annu. Rev. Plant Physiol. 38:467. However, other
methods are available to insert the $\Delta 6$ -desaturase genes
15 of the present invention into plant cells. Such
alternative methods include biolistic approaches (Klein
et al. (1987) Nature 327, 70), electroporation,
chemically-induced DNA uptake, and use of viruses or
pollen as vectors.

20 When necessary for the transformation method,
the $\Delta 6$ -desaturase genes of the present invention can be
inserted into a plant transformation vector, e.g. the
binary vector described by Bevan (1984) Nucleic Acids
Res. 12, 8111. Plant transformation vectors can be
25 derived by modifying the natural gene transfer system of
Agrobacterium tumefaciens. The natural system comprises
large Ti (tumor-inducing)-plasmids containing a large
segment, known as T-DNA, which is transferred to

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Surface-sterilized leaf disks are inoculated with the "disarmed" foreign DNA-containing *A. tumefaciens*, cultured for two days, and then transferred to antibiotic-containing medium. Transformed shoots are selected after rooting in medium containing the appropriate antibiotic, transferred to soil and regenerated.

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well-known to one of ordinary skill in the art (e.g.
1 Horsch et al. (1985) Science 227, 1129). In a preferred
embodiment, the transgenic plant is sunflower, oil seed
rape, maize, tobacco, peanut or soybean. Since progeny
of transformed plants inherit the DNA encoding $\Delta 6$ -
5 desaturase, seeds or cuttings from transformed plants
are used to maintain the transgenic plant line.

The present invention further provides a
method for providing transgenic plants with an increased
content of GLA. This method includes introducing DNA
10 encoding $\Delta 6$ -desaturase into plant cells which lack or
have low levels of GLA but contain LA, and regenerating
plants with increased GLA content from the transgenic
cells. In particular, commercially grown crop plants
are contemplated as the transgenic organism, including,
15 but not limited to, sunflower, soybean, oil seed rape,
maize, peanut and tobacco.

The present invention further provides a
method for providing transgenic organisms which contain
GLA. This method comprises introducing DNA encoding $\Delta 6$ -
20 desaturase into an organism which lacks or has low
levels of GLA, but contains LA. In another embodiment,
the method comprises introducing one or more expression
vectors which comprise DNA encoding $\Delta 12$ -desaturase and
 $\Delta 6$ -desaturase into organisms which are deficient in both
25 GLA and LA. Accordingly, organisms deficient in both LA
and GLA are induced to produce LA by the expression of
 $\Delta 12$ -desaturase, and GLA is then generated due to the
expression of $\Delta 6$ -desaturase. Expression vectors

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comprising DNA encoding $\Delta 12$ -desaturase, or $\Delta 12$ -
1 desaturase and $\Delta 6$ -desaturase, can be constructed by
methods of recombinant technology known to one of
ordinary skill in the art (Sambrook *et al.*, 1989) and
the published sequence of $\Delta 12$ -desaturase (Wada *et al*
5 [1990] Nature (London) 347, 200-203. In addition, it
has been discovered in accordance with the present
invention that nucleotides 2002-3081 of SEQ. ID NO:1
encode cyanobacterial $\Delta 12$ -desaturase. Accordingly, this
sequence can be used to construct the subject expression
10 vectors. In particular, commercially grown crop plants
are contemplated as the transgenic organism, including,
but not limited to, sunflower, soybean, oil seed rape,
maize, peanut and tobacco.

The present invention is further directed to a
15 method of inducing chilling tolerance in plants.
Chilling sensitivity may be due to phase transition of
lipids in cell membranes. Phase transition temperature
depends upon the degree of unsaturation of fatty acids
in membrane lipids, and thus increasing the degree of
20 unsaturation, for example by introducing $\Delta 6$ -desaturase
to convert LA to GLA, can induce or improve chilling
resistance. Accordingly, the present method comprises
introducing DNA encoding $\Delta 6$ -desaturase into a plant
cell, and regenerating a plant with improved chilling
25 resistance from said transformed plant cell. In a
preferred embodiment, the plant is a sunflower, soybean,
oil seed rape, maize, peanut or tobacco plant.

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The following examples further illustrate the
1 present invention.

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EXAMPLE 1

Strains and Culture Conditions

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Synechocystis (PCC 6803, ATCC 27184), Anabaena (PCC 7120, ATCC 27893) and Synechococcus (PCC 7942, ATCC 33912) were grown photoautotrophically at 30°C in BG11N+ medium (Rippka et al. [1979] J. Gen. Microbiol. 111, 1-61) under illumination of incandescent lamps ($60\mu\text{E}\cdot\text{m}^{-2}\cdot\text{S}^{-1}$). Cosmids and plasmids were selected and propagated in Escherichia coli strain DH5 α on LB medium supplemented with antibiotics at standard concentrations as described by Maniatis et al. (1982) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring, New York.

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EXAMPLE 2

1 Construction of Synechocystis Cosmid Genomic Library

5 Total genomic DNA from Synechocystis (PCC 6803) was partially digested with Sau3A and fractionated on a sucrose gradient (Ausubel et al. [1987] Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, New York). Fractions containing 30 to 40 kb DNA fragments were selected and ligated into the dephosphorylated BamHI site of the
10 cosmid vector, pDUCA7 (Buikema et al. [1991] J. Bacteriol. 173, 1879-1885). The ligated DNA was packaged in vitro as described by Ausubel et al. (1987), and packaged phage were propagated in E. coli DH5 α containing the AvaI and Eco4711 methylase helper
15 plasmid, pRL528 as described by Buikema et al. (1991). A total of 1152 colonies were isolated randomly and maintained individually in twelve 96-well microtiter plates.

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EXAMPLE 3

Gain-of-Function Expression of GLA in Anabaena

Anabaena (PCC 7120), a filamentous cyanobacterium, is deficient in GLA but contains significant amounts of linoleic acid, the precursor for GLA (Figure 2; Table 2). The Synechocystis cosmid library described in Example 2 was conjugated into Anabaena (PCC 7120) to identify transconjugants that produce GLA. Anabaena cells were grown to mid-log phase in BG11N+ liquid medium and resuspended in the same medium to a final concentration of approximately 2×10^8 cells per ml. A mid-log phase culture of E. coli RP4 (Burkardt et al. [1979] J. Gen. Microbiol. 114, 341-348) grown in LB containing ampicillin was washed and resuspended in fresh LB medium. Anabaena and RP4 were then mixed and spread evenly on BG11N+ plates containing 5% LB. The cosmid genomic library was replica plated onto LB plates containing 50 µg/ml kanamycin and 17.5 µg/ml chloramphenicol and was subsequently patched onto BG11N+ plates containing Anabaena and RP4. After 24 hours of incubation at 30°C, 30 µg/ml of neomycin was underlaid; and incubation at 30°C was continued until transconjugants appeared.

Individual transconjugants were isolated after conjugation and grown in 2 ml BG11N+ liquid medium with 15 µg/ml neomycin. Fatty acid methyl esters were prepared from wild type cultures and cultures containing pools of ten transconjugants as follows. Wild type and

transgenic cyanobacterial cultures were harvested by
1 centrifugation and washed twice with distilled water.
Fatty acid methyl esters were extracted from these
cultures as described by Dahmer *et al.* (1989) J. Amer.
Oil. Chem. Soc. 66, 543-548 and were analyzed by Gas
5 Liquid Chromatography (GLC) using a Tracor-560 equipped
with a hydrogen flame ionization detector and capillary
column (30 m x 0.25 mm bonded FSOT Superox II, Alltech
Associates Inc., IL). Retention times and co-
chromatography of standards (obtained from Sigma
10 Chemical Co.) were used for identification of fatty
acids. The average fatty acid composition was
determined as the ratio of peak area of each C18 fatty
acid normalized to an internal standard.

Representative GLC profiles are shown in Fig.
15 2. C18 fatty acid methyl esters are shown. Peaks were
identified by comparing the elution times with known
standards of fatty acid methyl esters and were confirmed
by gas chromatography-mass spectrometry. Panel A
depicts GLC analysis of fatty acids of wild type
20 Anabaena. The arrow indicates the migration time of
GLA. Panel B is a GLC profile of fatty acids of
transconjugants of Anabaena with pAM542+1.8F. Two GLA
producing pools (of 25 pools representing 250
transconjugants) were identified that produced GLA.
25 Individual transconjugants of each GLA positive pool
were analyzed for GLA production; two independent
transconjugants, AS13 and AS75, one from each pool, were
identified which expressed significant levels of GLA and

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which contained cosmids, cSy13 and cSy75, respectively
1 (Figure 3). The cosmids overlap in a region
approximately 7.5 kb in length. A 3.5 kb NheI fragment
of cSy75 was recloned in the vector pDUCA7 and
transferred to Anabaena resulting in gain-of-function
5 expression of GLA (Table 2).

Two NheI/Hind III subfragments (1.8 and 1.7
kb) of the 3.5 kb Nhe I fragment of cSy75-3.5 were
subcloned into "pBLUESCRIPT" (Stratagene) (Figure 3) for
sequencing. Standard molecular biology techniques were
10 performed as described by Maniatis et al. (1982) and
Ausubel et al. (1987). Dideoxy sequencing (Sanger et al.
[1977] Proc. Natl. Acad. Sci. USA 74, 5463-5467) of
pBS1.8 was performed with "SEQUENASE" (United States
Biochemical) on both strands by using specific
15 oligonucleotide primers synthesized by the Advanced DNA
Technologies Laboratory (Biology Department, Texas A & M
University). DNA sequence analysis was done with the
GCG (Madison, WI) software as described by Devereux et
al. (1984) Nucleic Acids Res. 12, 387-395.

20 Both NheI/HindIII subfragments were
transferred into a conjugal expression vector, AM542, in
both forward and reverse orientations with respect to a
cyanobacterial carboxylase promoter and were introduced
into Anabaena by conjugation. Transconjugants
25 containing the 1.8 kb fragment in the forward
orientation (AM542-1.8F) produced significant quantities
of GLA and octadecatetraenoic acid (Figure 2; Table 2).
Transconjugants containing other constructs, either

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reverse oriented 1.8 kb fragment or forward and reverse
1 oriented 1.7 kb fragment, did not produce detectable
levels of GLA (Table 2).

Figure 2 compares the C18 fatty acid profile
of an extract from wild type Anabaena (Figure 2A) with
5 that of transgenic Anabaena containing the 1.8 kb
fragment of cSy75-3.5 in the forward orientation (Figure
2B). GLC analysis of fatty acid methyl esters from
AM542-1.8F revealed a peak with a retention time
identical to that of authentic GLA standard. Analysis
10 of this peak by gas chromatography-mass spectrometry
(GC-MS) confirmed that it had the same mass
fragmentation pattern as a GLA reference sample.
Transgenic Anabaena with altered levels of
polyunsaturated fatty acids were similar to wild type in
15 growth rate and morphology.

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EXAMPLE 4

1 Transformation of Synechococcus
 with $\Delta 6$ and $\Delta 12$ Desaturase Genes

5 A third cosmid, cSy7, which contains a $\Delta 12$ -
desaturase gene, was isolated by screening the
Synechocystis genomic library with a oligonucleotide
synthesized from the published Synechocystis $\Delta 12$ -
desaturase gene sequence (Wada et al. [1990] Nature
10 (London) 347, 200-203). A 1.7 kb AvaI fragment from
this cosmid containing the $\Delta 12$ -desaturase gene was
identified and used as a probe to demonstrate that cSy13
not only contains a $\Delta 6$ -desaturase gene but also a $\Delta 12$ -
desaturase gene (Figure 3). Genomic Southern blot
analysis further showed that both the $\Delta 6$ -and $\Delta 12$ -
15 desaturase genes are unique in the Synechocystis genome
so that both functional genes involved in C18 fatty acid
desaturation are linked closely in the Synechocystis
genome.

20 The unicellular cyanobacterium Synechococcus
(PCC 7942) is deficient in both linoleic acid and
GLA(3). The $\Delta 12$ and $\Delta 6$ -desaturase genes were cloned
individually and together into pAM854 (Bustos et al.
[1991] J. Bacteriol. 174, 7525-7533), a shuttle vector
that contains sequences necessary for the integration of
25 foreign DNA into the genome of Synechococcus (Golden et
al. [1987] Methods in Enzymol. 153, 215-231).
Synechococcus was transformed with these gene constructs
and colonies were selected. Fatty acid methyl esters

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1 were extracted from transgenic Synechococcus and
analyzed by GLC.

5 Table 2 shows that the principal fatty acids
of wild type Synechococcus are stearic acid (18:0) and
oleic acid (18:1). Synechococcus transformed with
pAM854- Δ 12 expressed linoleic acid (18:2) in addition to
the principal fatty acids. Transformants with pAM854- Δ 6
and Δ 12 produced both linoleate and GLA (Table 1).
These results indicated that Synechococcus containing
both Δ 12- and Δ 6-desaturase genes had gained the
10 capability of introducing a second double bond at the
 Δ 12 position and a third double bond at the Δ 6 position
of C18 fatty acids. However, no changes in fatty acid
composition was observed in the transformant containing
pAM854- Δ 6, indicating that in the absence of substrate
15 synthesized by the Δ 12 desaturase, the Δ 6-desaturase is
inactive. This experiment further confirms that the 1.8
kb NheI/HindIII fragment (Figure 3) contains both coding
and promoter regions of the Synechocystis Δ 6-desaturase
gene. Transgenic Synechococcus with altered levels of
20 polyunsaturated fatty acids were similar to wild type in
growth rate and morphology.

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TABLE 2

Composition of C18 Fatty Acids in Wild Type and Transgenic Cyanobacteria

Strain	Fatty acid (%)					
	18:0	18:1	18:2	18:3(α)	18:3(γ)	18:4
Wild Type						
<i>Synechocystis</i> (sp. PCC6803)	13.6	4.5	54.5	—	27.3	—
<i>Anabaena</i> (sp. PCC7120)	2.9	24.8	37.1	35.2	—	—
<i>Synechococcus</i> (sp. PCC7942)	20.6	79.4	—	—	—	—
<i>Anabaena</i> Transcon-						
stants						
cy75	3.8	24.4	22.3	9.1	27.9	12.5
cy75-3.5	4.3	27.6	18.1	3.2	40.4	6.4
PAM542 - 1.8F	4.2	13.9	12.1	19.1	25.4	25.4
PAM542 - 1.8R	7.7	23.1	38.4	30.8	—	—
PAM542 - 1.7F	2.8	27.8	36.1	33.3	—	—
PAM542 - 1.7R	2.8	25.4	42.3	29.6	—	—
<i>Synechococcus</i> Trans-						
stants						
PAM854	27.8	72.2	—	—	—	—
PAM854 - Δ ¹²	4.0	43.2	46.0	—	—	—
PAM854 - Δ ⁶	18.2	81.8	—	—	—	—
PAM854 - Δ ⁶ & Δ ¹²	42.7	25.3	19.5	—	16.5	—

18:0, stearic acid; 18:1, oleic acid; 18:2, linoleic acid; 18:3(α), α-linolenic acid; 18:3(γ), γ-linolenic acid; 18:4, octadecatetraenoic acid

EXAMPLE 5

Nucleotide Sequence of $\Delta 6$ -D saturase

1 The nucleotide sequence of the 1.8 kb fragment
of cSy75-3.5 including the functional $\Delta 6$ -desaturase gene
5 was determined. An open reading frame encoding a
polypeptide of 359 amino acids was identified (Figure
4). A Kyte-Doolittle hydropathy analysis (Kyte et al.
[1982] J. Mol. Biol. 157, 105-132) identified two
regions of hydrophobic amino acids that could represent
10 transmembrane domains (Figure 1A); furthermore, the
hydropathic profile of the $\Delta 6$ -desaturase is similar to
that of the $\Delta 12$ -desaturase gene (Figure 1B; Wada et al.)
and $\Delta 9$ -desaturases (Thiede et al. [1986] J. Biol. Chem.
261, 13230-13235). However, the sequence similarity
15 between the Synechocystis $\Delta 6$ - and $\Delta 12$ -desaturases is
less than 40% at the nucleotide level and approximately
18% at the amino acid level.

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EXAMPLE 6

1 Transfer of Cyanobacterial Δ^6 -D saturase into Tobacco

5 The cyanobacterial Δ^6 -desaturase gene was mobilized into a plant expression vector and transferred to tobacco using Agrobacterium mediated gene transfer techniques. To ensure that the transferred desaturase is appropriately expressed in leaves and developing seeds and that the desaturase gene product is targeted to the endoplasmic reticulum or the chloroplast, various
10 expression cassettes with Synechocystis Δ -desaturase open reading frame (ORF) were constructed. Components of these cassettes include: (i) a 35S promoter or seed specific promoter derived from the sunflower helianthinin gene to drive $\Delta 6$ -desaturase gene expression
15 in all plant tissues or only in developing seeds respectively, (ii) a putative signal peptide either from carrot extension gene or sunflower helianthinin gene to target newly synthesized $\Delta 6$ -desaturase into the ER, (iii) an ER lumen retention signal sequence (KDEL) at
20 the COOH-terminal of the $\Delta 6$ -desaturase ORF, and (iv) an optimized transit peptide to target $\Delta 6$ desaturase into the chloroplast. The 35S promoter is a derivative of pRTL2 described by Restrepo et al. (1990). The optimized transit peptide sequence is described by Van
25 de Broeck et al. (1985). The carrot extensin signal peptide is described by Chen et al (1985) EMBO J. 2, 2145.

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Transgenic tobacco plants were produced containing a chimeric cyanobacterial desaturase gene, comprised of the Synechocystis $\Delta 6$ -desaturase gene fused to an endoplasmic reticulum retention sequence (KDEL) and extensin signal peptide driven by the CaMV 35S promoter. PCR amplifications of transgenic tobacco genomic DNA indicate that the $\Delta 6$ -desaturase gene was incorporated into the tobacco genome. Fatty acid methyl esters of leaves of these transgenic tobacco plants were extracted and analyzed by Gas Liquid Chromatography (GLC). These transgenic tobacco accumulated significant amounts of GLA (Figure 4). Figure 4 shows fatty acid methyl esters as determined by GLC. Peaks were identified by comparing the elution times with known standards of fatty acid methyl ester. Accordingly, cyanobacterial genes involved in fatty acid metabolism can be used to generate transgenic plants with altered fatty acid compositions.

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EXAMPLE 7

Construction of Borage cDNA library

1 Membrane bound polysomes were isolated from
borage seeds 12 days post pollination (12 DPP) using the
protocol established for peas by Larkins and Davies
5 (1975 Plant Phys. 55:749-756). RNA was extracted from
the polysomes as described by Mechler (1987 Methods in
Enzymology 152:241-248, Academic Press).

 Poly-A+ RNA was isolated from the membrane
bound polysomal RNA by use of Oligotex-dT beads
10 (Qiagen). Corresponding cDNA was made using
Stratagene's ZAP cDNA synthesis kit. The cDNA library
was constructed in the lambda ZAP II vector (Stratagene)
using the lambda ZAP II vector kit. The primary library
was packaged in Gigapack II Gold packaging extract
15 (Stratagene). The library was used to generate
expressed sequence tags (ESTs), and sequences
corresponding to the tags were used to scan the GenBank
database.

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EXAMPLE 8
Hybridization Protocol

1 Hybridization probes for screening the borage
cDNA library were generated by using random primed DNA
synthesis as described by Ausubel et al (1994 Current
5 Protocols in Molecular Biology, Wiley Interscience,
N.Y.) and corresponded to previously identified
abundantly expressed seed storage protein cDNAs.
Unincorporated nucleotides were removed by use of a G-50
spin column (Boehringer Mannheim). Probe was denatured
10 for hybridization by boiling in a water bath for 5
minutes, then quickly cooled on ice. Filters for
hybridization were prehybridized at 60°C for 2-4 hours
in prehybridization solution (6XSSC [Maniatis et al 1984
Molecular Cloning A Laboratory Manual, Cold Spring
15 Harbor Laboratory], 1X Denharts Solution, 0.05% sodium
pyrophosphate, 100 µg/ml denatured salmon sperm DNA).
Denatured probe was added to the hybridization solution
(6X SSC, 1X Denharts solution, 0.05% sodium
pyrophosphate, 100 µg/ml denatured salmon sperm DNA) and
20 incubated at 60°C with agitation overnight. Filters
were washed in 4x, 2x, and 1x SET washes for 15 minutes
each at 60°C. A 20X SET stock solution is 3M NaCl, 0.4
M Tris base, 20 mM Na₂EDTA-2H₂O. The 4X SET wash was 4X
SET, 12.5 mM PO₄, pH 6.8 and 0.2% SDS. The 2X SET wash
25 was 2X SET, 12.5 mM PO₄, pH 6.8 and 0.2% SDS. The 1X SET
wash was 1X SET, 12.5 mM PO₄, pH 6.8 and 0.2% SDS.
Filters were allowed to air dry and were then exposed to
X-ray film for 24 hours with intensifying screens at -
80°C.

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EXAMPLE 9

Random sequencing of cDNAs from a borage seed
(12 DPP) membrane-bound polysomal library

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The borage cDNA library was plated at low density (500 pfu on 150 mm petri dishes). Highly prevalent seed storage protein cDNAs were "subtracted" by screening with the previously identified corresponding cDNAs. Non-hybridizing plaques were excised using Stratagene's excision protocol and reagents. Resulting bacterial colonies were used to inoculate liquid cultures and were either sequenced manually or by an ABI automated sequencer. Each cDNA was sequenced once and a sequence tag generated from 200-300 base pairs. All sequencing was performed by cycle sequencing (Epicentre). Over 300 ESTs were generated. Each sequence tag was compared to GenBank database by BLASTX computer program and a number of lipid metabolism genes, including the $\Delta 6$ -desaturase were identified.

Database searches with a cDNA clone designated mbp-65 using BLASTX with the GenBank database resulted in a significant match to the Synechocystis $\Delta 6$ -desaturase. It was determined however, that this clone was not a full length cDNA. A full length cDNA was isolated using mbp-65 to screen the borage membrane-bound polysomal library. The sequence of the isolated cDNA was determined (Fig. 5A, SEQ ID NO:4) and the protein sequence of the open reading frame (Fig. 5B, SEQ ID NO:5) was compared to other known desaturases using Geneworks (IntelligGenetics) protein alignment program

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(Fig. 2). This alignment indicated that the cDNA was the borage $\Delta 6$ -desaturase gene.

1 Although similar to other known plant
desaturases, the borage delta 6-desaturase is distinct
as indicated in the dendrogram shown in Fig. 6.
Furthermore, comparison of the amino acid sequences
5 characteristic of desaturases, particularly those
proposed to be involved in metal binding (metal box 1
and metal box 2), illustrates the differences between
the borage delta 6-desaturase and other plant
desaturases (Table 3).

10 The borage delta 6-desaturase is distinguished
from the cyanobacterial form not only in over all
sequence (Fig. 6) but also in the lipid box, metal box 1
and metal box 2 amino acid motifs (Table 3). As Table 3
indicates, all three motifs are novel in sequence. Only
15 the borage delta 6-desaturase metal box 2 showed some
relationship to the Synechocystis delta-6 desaturase
metal box 2.

20 In addition, the borage delta 6-desaturase is
also distinct from another borage desaturase gene, the
delta-12 desaturase. P1-81 is a full length cDNA that
was identified by EST analysis and shows high similarity
to the Arabidopsis delta-12 desaturase (Fad 2). A
comparison of the lipid box, metal box 1 and metal box 2
amino acid motifs (Table 3) in borage delta 6 and delta-
25 12 desaturases indicates that little homology exists in
these regions. The placement of the two sequences in
the dendrogram in Fig. 6 indicates how distantly related
these two genes are.

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Table 3. Comparison of common amino acid motifs in membrane-bound desaturases

Desaturase	Lipid Box	Amino Acid Motif	
		Metal Box 1	Metal Box 2
Borage Δ^6	WIGHDAGH (SEQ. ID. NO: 6)	HNAHH (SEQ. ID. NO: 12)	FQIEHH (SEQ. ID. NO: 20)
Synechocystis Δ^6	NVGH DANH (SEQ. ID. NO: 7)	HNYLHH (SEQ. ID. NO: 13)	HQVTHH (SEQ. ID. NO: 21)
Arab. chloroplast Δ^{15}	VLGHDCGH (SEQ. ID. NO: 8)	HRTHH (SEQ. ID. NO: 14)	HVIHH (SEQ. ID. NO: 22)
Rice Δ^{15}	VLGHDCGH (SEQ. ID. NO: 8)	HRTHH (SEQ. ID. NO: 14)	HVIHH (SEQ. ID. NO: 22)
Glycine chloroplast Δ^{15}	VLGHDCGH (SEQ. ID. NO: 8)	HRTHH (SEQ. ID. NO: 14)	HVIHH (SEQ. ID. NO: 22)
Arab. fad3 (Δ^{15})	VLGHDCGH (SEQ. ID. NO: 8)	HRTHH (SEQ. ID. NO: 14)	HVIHH (SEQ. ID. NO: 22)
Brassica fad3 (Δ^{15})	VLGHDCGH (SEQ. ID. NO: 8)	HRTHH (SEQ. ID. NO: 14)	HVIHH (SEQ. ID. NO: 22)
Borage Δ^{12} (Pl-81)*	VIAHECGH (SEQ. ID. NO: 9)	HRRHH (SEQ. ID. NO: 15)	HVAHH (SEQ. ID. NO: 23)
Arab. fad2 (Δ^{12})	VIAHECGH (SEQ. ID. NO: 9)	HRRHH (SEQ. ID. NO: 15)	HVAHH (SEQ. ID. NO: 23)
Arab. chloroplast Δ^{12}	VIGHDCAH (SEQ. ID. NO: 10)	HDRHH (SEQ. ID. NO: 16)	HIPHH (SEQ. ID. NO: 24)
Glycine plastid Δ^{12}	VIGHDCAH (SEQ. ID. NO: 10)	HDRHH (SEQ. ID. NO: 16)	HIPHH (SEQ. ID. NO: 24)
Spinach plastidial n-6	VIGHDCAH (SEQ. ID. NO: 10)	HDQHH (SEQ. ID. NO: 17)	HIPHH (SEQ. ID. NO: 24)
Synechocystis Δ^{12}	VVGHDCGH (SEQ. ID. NO: 11)	HDHHH (SEQ. ID. NO: 18)	HIPHH (SEQ. ID. NO: 24)
Anabaena Δ^{12}	VLGHDCGH (SEQ. ID. NO: 8)	HNHHH (SEQ. ID. NO: 19)	HVPHH (SEQ. ID. NO: 25)

*Pl-81 is a full length cdna which was identified by EST analysis and shows high similarity to the Arbidopsis Δ^{12} desaturase (fad2)

EXAMPLE 10

**Construction of 222.1 Δ^6 NOS for transient
and expression**

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The vector pBI221 (Jefferson et al. 1987
EMBO J. 6:3901-3907) was prepared for ligation by
digestion with BamHI and EcoICR I (Promega) which
excises the GUS coding region leaving the 35S promoter
and NOS terminator intact. The borage Δ^6 -desaturase
cDNA was excised from the Bluescript plasmid
(Stratagene) by digestion with BamHI and XhoI. The
XhoI end was made blunt by use of the Klenow fragment.
This fragment was then cloned into the BamHI/EcoICR I
sites of pBI221, yielding 221.1 Δ^6 NOS (Fig. 7). In
221.1 Δ^6 .NOS, the remaining portion (backbone) of the
restriction map depicted in Fig. 7 is pBI221.

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EXAMPLE 11

Construction of 121.1 Δ^6 .NOS for stable transformation

1 The vector pBI121 (Jefferson et al. 1987
EMBO J. 6:3901-3907) was prepared for ligation by
digestion with BamHI and EcoICR I (Promega) which
5 excises the GUS coding region leaving the 35S promoter
and NOS terminator intact. The borage Δ^6 -desaturase
cDNA was excised from the Bluescript plasmid
(Stratagene) by digestion with BamHI and XhoI. The
XhoI end was made blunt by use of the Klenow fragment.
10 This fragment was then cloned into the BamHI/EcoICR I
sites of pBI121, yielding 121.1 Δ^6 NOS (Fig. 7). In
121. Δ^6 .NOS, the remaining portion (backbone) of the
restriction map depicted in Fig. 7 is pBI121.

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EXAMPLE 12
Transient Expression

1 All work involving protoplasts was performed
in a sterile hood. One ml of packed carrot suspension
cells were digested in 30 mls plasmolyzing solution
5 (25 g/l KCl, 3.5 g/l CaCl₂·H₂O, 10mM MES, pH 5.6 and
0.2 M mannitol) with 1% cellulase, 0.1% pectolyase,
and 0.1% dreisalase overnight, in the dark, at room
temperature. Released protoplasts were filtered
through a 150 µm mesh and pelleted by centrifugation
10 (100x g, 5 min.) then washed twice in plasmolyzing
solution. Protoplasts were counted using a double
chambered hemocytometer. DNA was transfected into the
protoplasts by PEG treatment as described by Nunberg
and Thomas (1993 Methods in Plant Molecular Biology
15 and Biotechnology, B.R. Glick and J.E. Thompson, eds.
pp. 241-248) using 10⁶ protoplasts and 50-70 ug of
plasmid DNA (221.Δ6.NOS). Protoplasts were cultured
in 5 mls of MS media supplemented with 0.2M mannitol
and 3 µm 2,4-D for 48 hours in the dark with shaking.

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EXAMPLE 13

Stable transformation of tobacco

1 121.1Δ⁶NOS plasmid construction was used to
transform tobacco (*Nicotiana tabacum* cv. xanthi) via
5 Agrobacterium according to standard procedures (Horsh
et al., 1985 Science 227: 1229-1231; Bogue et al.,
1990 Mol. Gen. Genet. 221:49-57), except that initial
transformants were selected on 100 ug/ml kanamycin.

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EXAMPLE 14

Preparation and analysis of fatty acid methyl esters (FAMES)

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5 Tissue from transfected protoplasts and
transformed tobacco plants was frozen in liquid
nitrogen and lyophilized overnight. FAMES were
prepared as described by Dahmer et al (1989 J. Amer.
Oil Chem. Soc. 66:543-548). In some cases, the
solvent was evaporated again, and the FAMES were
resuspended in ethyl acetate and extracted once with
deionized water to remove any water soluble
10 contaminants. The FAMES were analyzed by gas
chromatography (GC) on a J&W Scientific DB-wax column
(30 m length, 0.25 mm ID, 0.25 μ m film).

15 An example of a transient assay is shown in
Fig. 8 which represents three independent
transfections pooled together. The addition of the
borage Δ 6-desaturase cDNA corresponds with the
appearance of gamma linolenic acid (GLA) which is one
of the possible products of Δ 6-desaturase.
Furthermore, transgenic tobacco containing the borage
20 Δ 6-desaturase driven by the cauliflower mosaic virus
35S promoter also produce GLA as well as octa-
decanoic acid (18:4) which is formed by the further
desaturation of GLA (Fig. 9). These results indicate
that the borage delta 6-desaturase gene can be used to
25 transform plant cells to achieve altered fatty acid
compositions.

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EXAMPLE 15

Isolation of an Evening Primrose $\Delta 6$ -desaturase gene

1 Total RNA was isolated from evening primrose embryos using the method of Chang, Puryear, and Cairney (1993) *Plant Mol Biol Reporter* 11:113-116.

5 Poly A⁺ RNA was selected on oligotex beads (Qiagen) and used as a template for cDNA synthesis. The cDNA library was constructed in the lambda ZAP II vector (Stratagene) using the lambda ZAP II vector kit. The primary library was packaged with Gigapack II Gold packaging extract (Stratagene).

10 PCR primers based on sequences in the borage $\Delta 6$ -desaturase gene were synthesized by a commercial source using standard protocols and included the following oligonucleotides:

15 5' AAACCAATCCATCCAAGRA 3' SEQ ID NO:27

5' KTGGTGGAAATGGAMSCATAA 3' SEQ ID NO:28

(R=A and G, K=G and T, M=A and C, S=G and C)

20 A primer that matches a region that flanks the insertion site of the lambda ZAP II vector was also synthesized using an ABI394 DNA synthesizer and standard protocols. This primer had the following sequence:

5' TCTAGAACTAGTGGATC 3' SEQ ID NO:29

25 An aliquot of the cDNA library was used directly as template in a PCR reaction using SEQ ID NO: 27 and SEQ ID NO:29 as primers. The reactions were carried out in a volume of 50 μ l using an annealing temperature of 50°C for 2 minutes, an

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extension temperature of 72°C for 1.5 minutes, and a
melting temperature of 94°C for 1 minute for 29
cycles. A final cycle with a 2 minute annealing at
50°C and a 5 minute extension at 72°C completed the
reaction. One µl from this reaction was used as a
template in a second reaction using the same
conditions except that the primers were SEQ ID NO:27
and SEQ ID NO:28. A DNA fragment of predicted size
based on the location of the primer sequences in the
the borage Δ6-desaturase cDNA was isolated.

This PCR fragment was cloned into pT7 Blue
(Novagen) and used to screen the evening primrose cDNA
library at low stringency conditions: The
hybridization buffer used was 1% bovine serum albumin
(crystalline fraction V), 1mM EDTA, 0.5 M NaHPO₄ pH7.2,
and 7% SDS. The hybridizations were at 65°C. The
wash buffer was 1mM Na₂EDTA, 40 mM NaHPO₄ pH7.2 and 1%
SDS. Primary screens were washed at 25°C. Secondary
and tertiary screens were washed at 25°C, 37°C, and
42°C. One of the positively hybridizing clones that
was identified in the evening primrose cDNA library
was excised as a phagemid in pBluescript. The DNA
sequence of the 1687 bp insert of this phagemid
(pIB9748-4) was determined (Fig. 10, SEQ ID NO: 26)
using the ABIPRISM™ dye terminator cycle sequencing
core kit from Perkin Elmer according to the
manufacturer's protocol. The sequence encodes a full
length protein of 450 amino acids (SEQ ID NO:27) with
a molecular weight of 51492 daltons.

Alignment of the deduced amino acid sequence
with that of borage Δ6-desaturase was performed using

1 the Geneworks program (Fig. 11). The evening primrose
2 $\Delta 6$ -desaturase protein is identical at 58% of the
3 residues and similar at an additional 20% of the
4 residues. Only two small gaps, near the carboxy
5 terminal end of the protein were introduced by the
6 program to obtain the alignment (Fig. 11). The two
7 proteins were compared using two different algorithms
8 that measure the hydrophobicity of regions to the
9 protein. Figures 12A and 12B are Kyte-Doolittle
10 hydrophobicity plots of borage $\Delta 6$ -desaturase and
11 evening primrose $\Delta 6$ -desaturase, respectively.
12 Figures 13A and 13B are Hopwood hydrophobicity plots
13 generated in the program DNA Strider for the same
14 proteins. A discussion of the algorithm used to
15 generate these plots can be found in Hopp, T.P. and
16 Woods, K.R. 1983 Molecular Immunology 20:483-89.
17 Substantial similarity exists between the borage and
18 evening primrose proteins using either algorithm.
19 TMPredict, a program that predicts the location of
20 transmembrane regions of proteins was run on the two
21 sequences and again similar results were obtained
22 (Figures 14 and 15). Several weights matrices are used
23 in scoring the predictions as reported in Hofmann, K.
24 and Stoffel, W. 1993 *Biol. C. Hoppe-Scyler* 347:156.
25 Positive values (x-axis) greater than 500 are
26 considered significant predictors of a membrane
27 spanning region; the x-axis represents the linear
28 amino acid sequences.

29 The membrane bound desaturases of plants
30 possess three histidine rich motifs (HRMs). These
31 motifs are identified in the evening primrose

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sequence and are indicated in Figure 10 by underlined
plain text. The motifs in this sequence were
1 identical to those found in borage $\Delta 6$ -desaturase with
the exception of those that are italicized (S 161 and
L374). The borage $\Delta 6$ -desaturase is unique among known
membrane bound desaturases in having a cytochrome b5
5 domain at the carboxy terminal end. The evening
primrose protein encoded by pIB9748-4 also has this
domain. The heme binding motif of cytochrome b5
proteins is indicated in Figure 10 by underlined bold
text.

10 These data indicate that a $\Delta 6$ -desaturase
cDNA from evening primrose has been isolated and
characterized.

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EXAMPLE 16

**Construction of expression vectors for transient and
1 stable expression of an evening primrose $\Delta 6$ -desaturase**

The evening primrose $\Delta 6$ -desaturase cDNA is
excised from the Bluescript phagemid by digestion with
5 Xba I and Xho I. The entire cDNA sequence including
the 5' transcribed but untranslated region depicted in
Figure 10 (SEQ ID NO:26) is operably linked to any one
of various promoters and/or other regulatory elements
in an expression vector, in order to effect
10 transcription and translation of the $\Delta 6$ -desaturase
gene. Alternatively, the cDNA sequence depicted in
Figure 10 may be trimmed at the 5' end so that the 5'
transcribed but untranslated sequence is removed. The
A of the ATG translational start codon is then made
15 the first nucleotide following the promoter and/or
other regulatory sequence in an expression vector.

In order to express the subject evening
primrose cDNA in pBI221 (Jefferson et al. 1987 EMBO J.
6:3901-3907) the following manipulations are
20 performed:

The plasmid pBI221 is digested with EcoICR I
(Promega) or Ecl 136 II (NEB) and Xba I which excises
the GUS coding region and leaves the 35S promoter and
NOS terminator intact. The evening primrose $\Delta 6$ -
25 desaturase cDNA is excised from pIB9748-4 by digestion
with Xba I and Xho I. The Xho I end is made blunt by
use of the Klenow fragment. The excised gene is then
cloned into the cloned into the Xba I/Eco ICR I sites
of pBI221. The resulting construct is then

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transfected into carrot protoplasts. One ml of packed carrot suspension cells are digested in 30 ml of plasmolyzing solution (25 g/l KCl 3.5 g/l $\text{CaCl}_2 \cdot \text{H}_2\text{O}$, 10 mM MES, pH 5.6 and 0.2 M mannitol) with 1% cellulase 0.1% pectolyase, and 0.1% dreisalase overnight, in the dark, at room temperature. Released protoplasts are filtered through a 150 μm mesh and pelleted by centrifugation (100 x g, 5 minutes), then washed twice in plasmolyzing solution. Protoplasts are counted using a double chambered hemocytometer. DNA is transfected into the protoplasts by PEG treatment as described by Nunberg and Thomas (1993 Methods in Plant Molecular Biology and Biotechnology, B.R. Glick and J.E. Thompson, eds. pp 241-248) using 10^6 protoplasts and 50-70 μg of DNA from the above construct. Protoplasts are cultured in 5 ml of MS medium supplemented with 0.2 M mannitol and 3 μM 2, 4-D for 48 hours in the dark with shaking. Tobacco is transformed with the same $\Delta 6$ -desaturase expression construct by following the method of Example 13.

In order to express the subject evening primrose cDNA in pBI121 (Jefferson et al. 1987 EMLBO J. 6:3901-3907), the following manipulations are performed:

The plasmid pBI121 is digested with EcoICR I (Promega) or Ecl 136 II (NEB) and Xba I which excises the GUS coding region and leaves the 35S promoter and NOS terminator intact. The evening primrose $\Delta 6$ -desaturase cDNA is excised from pIB9748-4 by digestion with Xba I and Xho I. The Xho I end is made blunt by use of the Klenow fragment. The excised gene is then

cloned into the Xba I/Eco ICR I sites of pBI121. The
resulting construct is used to transform *Arabidopsis*
1 *thaliana* via *Agrobacterium* according to standard
protocols (Bechtold N., Ellis. J., and Pelletier, G
1993 C.R. Acad Sci Paris 316:1194-1199). Carrot and
tobacco are transformed as described above.

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